

Figure 1

human  
tezi  
EST2  
p123

Motif 0

AKFLHWLHLSVYVVELLRSPFFYVTETTPQKNR  
 ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSPIIPILQSFFYITSSSDLRNR  
 LXDFRWLFISD---IWFTKHNFEENLNQLAICFISWLPRLIPKIIQTFFYCTEISSTVT-  
 TREISWMQVET-SAXHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK  
 . . . . .

human  
tezi  
EST2  
p123

Motif 1

LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DOL  
 TVYFRKDIWKLLCRPFI-TSMKHEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--STP  
 IVYFRHDTWNKLITPFIIVEYFKTYLVENMVCRNHNSTLS--HFNHSHKRIIPKKSNEF  
 TYYRKNIDVIMKHSI-ADLKKETLAEVQSEKVBWKKK-LGFAPGKLRLIPKK--TTF  
 . . . . .

human  
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EST2  
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Motif 2

RPIVNMDDYVVGARTFRREKRAERLTSRVKALP-SVLNYERA  
 RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF  
 RIIAIPCRGADEEEFTIYKENHKMAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF  
 RPIHTFNKKIVNSDRKTTKLTTNTKLLNSHLMKTLKN-RMFKDPPGPAVFHYDDVMKKY  
 . . . . .

tezi  
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p123

Motif 3 (A)

KKDLLKHRMFOR-KXYFVRIDIKSCYDRIKQDLHFRIVKK-KLXDPEPVIRKYATIHATS  
 XQRLKKFNNVLPZLYFMKFDVKS CYDSIPRMECHRILKD-ALKNENGFFVRSQYFFFTN  
 ZEFVCKWKQVGPPLFFATHDIEKCYDSVNREKLSTFLKTTXLLSSDFWIHTAQILKRKY  
 . . . . .

264780-15621680

Figure 2

454T80" T562T680

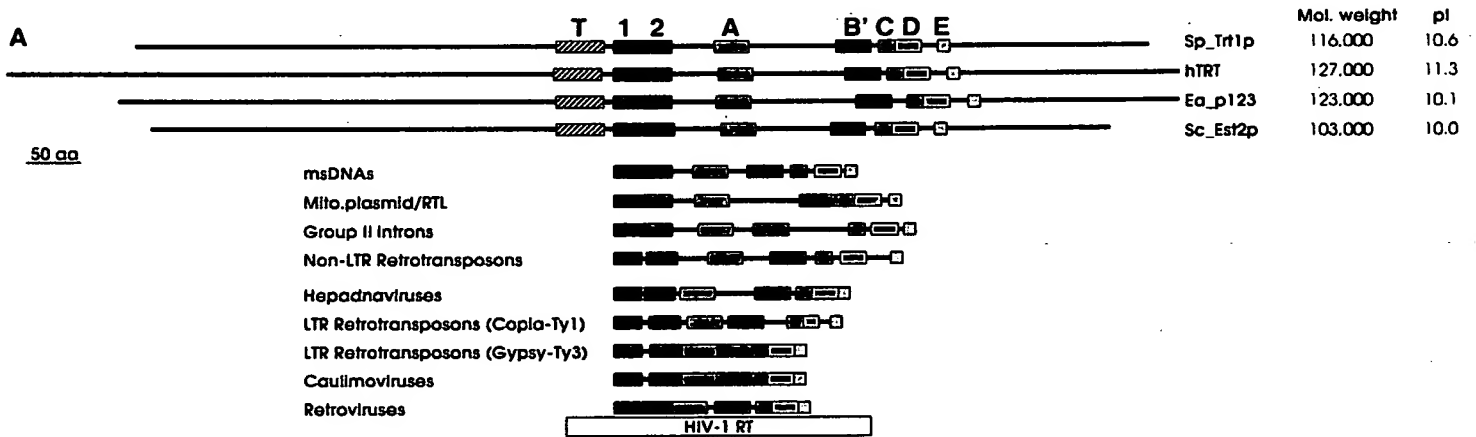
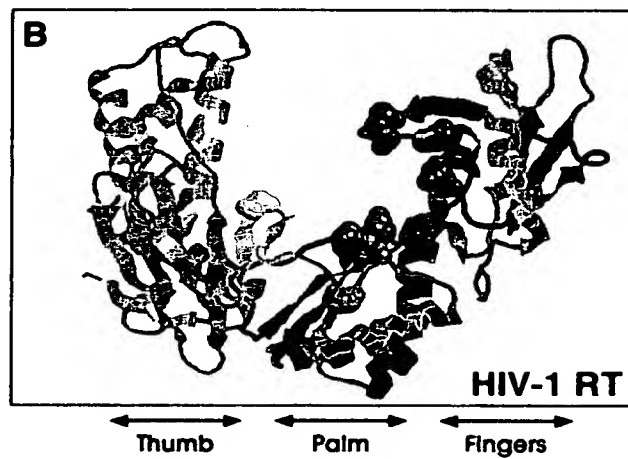


Figure 3



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Figure 4

C

Motif T		
TRT con	WL hh hh pFFY TE p p Y RK W L h I K	
Sp_Trt1p	429 WLYNSFIIPILQSFYITESSDLNRRTVYFRKDIWKLLCRPFITSMKM	8
hTRT	546 WLMSVYVVELLRSPFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLE	10
Se_p123	441 WIFEDLVVSLIRCFYVTEQOKSYSKTYRKNIVDVMKMSIADLKE	8
Sc_Est2p	366 WLPRQLIPKIIQTFFYCTEISSTVT-IVYFRHDIWNKLITPPIVEYFK	8

Motif 1			Motif 2			Motif A		
TRT con	h hrhIPKK p		FRhI h h	K		PcLYFh hdh CYD I	hhK K	
Sp_Trt1p	NNVRMDTQKTTLPPIVIRLLPKKNT-	0	FRITNLRRKFLIKMGSNKMLVSTNQTL	40	FGRKKYFVRIDIKSCYDRIKQDLMFRIVEKKLEK	82		
hTRT	EVRQHRARPALLTSRLRFIPKPDG-	0	LRPIVNDYVVGARTFRREKRAERLTSRV	45	PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP	87		
Se_p123	KEVEEWKKSGLFAPGKLRLLIPKTT-	0	FRPIMTFNKKIVNSDRKTKLTNTKLLN	41	GQPKLFTATMDIEKCYDSVNREKLTSTFKTTKLL	100		
Sc_Est2p	CRNHNSYTLNFNHSMRIIPKSN	1	FRIIAIPCRGADEEFTIYKENHNKNAIQP	42	VLPELYFMKPDVKSCYDSIPRMECMRILEDALEN	68		

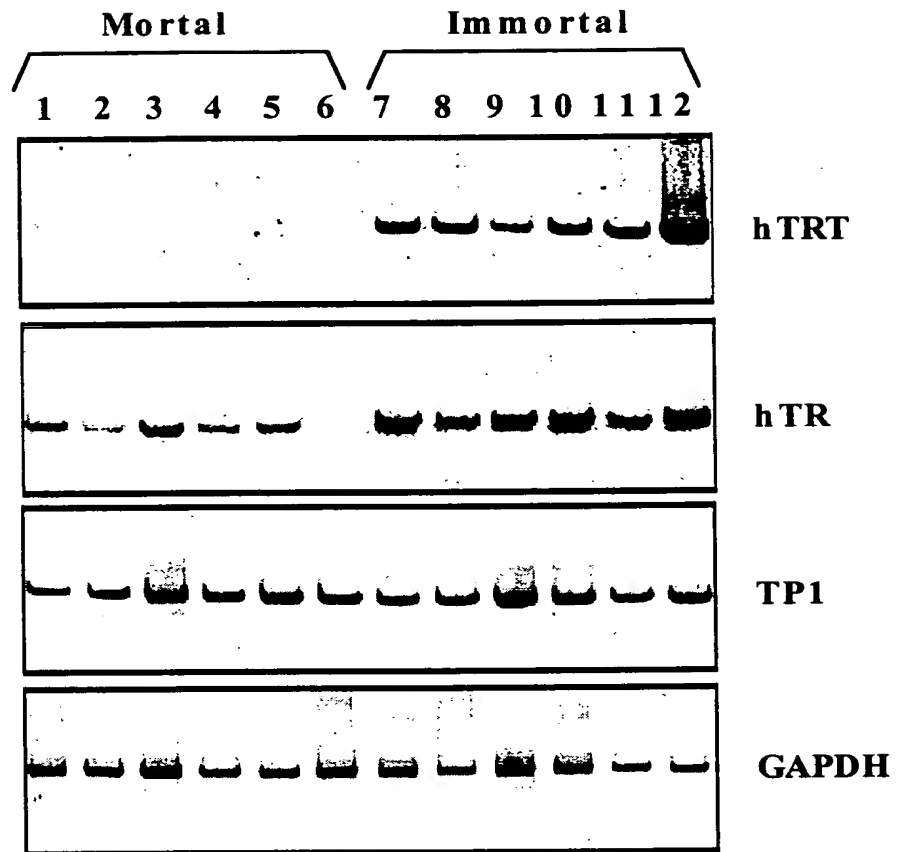
  

Motif B'			Motif C			Motif D			Motif E		
TRT con	K Y Q GIPQGS LS hL h Y DL	F	LLRL DDPLHIT	A F h G c p N cK		W G S					
Sp_Trt1p	SOYLQKVQIPQGSILSSFLCHFYMEDLIDEYLSFT	6	LLRVVDDFLFITVNNKD	0	AKKFLNLSLRGPEKHNFTSLERTVI	17	KKRMPFFQFSV	181			
hTRT	KSYVQCQGIPQGSILSTLLCSLCYGD MENKLFAGI	5	LLRLVDDFLVTPHLTH	0	AKTFLRLTVRGVPEYGCVVNLKRTVV	19	HGLFPWCGLLL	197			
Se_p123	KFYKQTKGIPQGLCVSSILSSFYATLEESSLGFL	14	LMRLTDDYLLITTQENN	0	AVLFIEKLINVSRENGPKFPMKRLQT	23	QDYCDWISISI	179			
Sc_Est2p	KCYIREDLQFGSSLSAPIVDLVYDDLLEFYSEFK	8	ILKLADDPLIISTDQQO	0	VINIKKLAMGGFQKYNKANKRDKILA	20	KELEVWKHSBT	146			

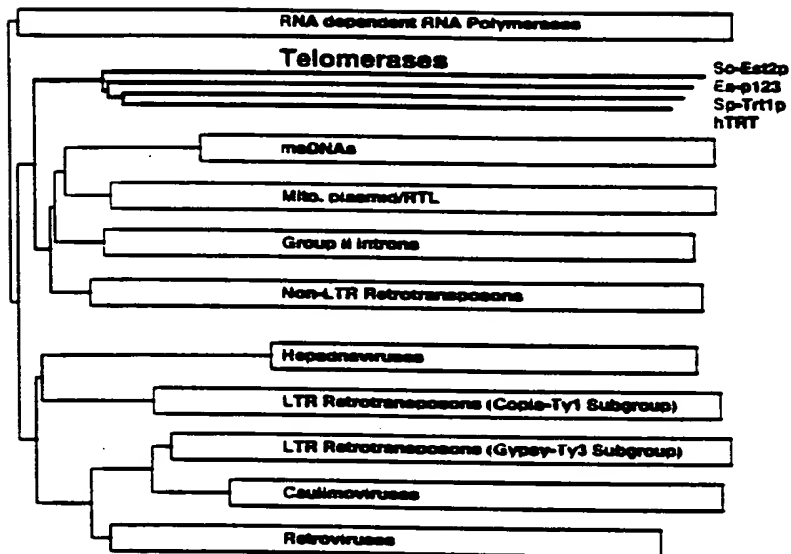
Motif B			Motif C			Motif D			Motif E		
TRT con	hPQG pP hh h		h Y DDhhh	Gh h cK h		hLG h					
Sp_Trt1p	TYHKPMLQLPQGSLSIPILCNIVMTLVDNWLEDYI	55	VVRYADDILIGVLGSKN	2	KMIKRDNLNPLNS-LGLTMNEERTLI	4	ETPARFLGYNI				
hTRT	RAGQICAGVPGGSNLGPILYSIFSSDMP LPHIYHP	7	LSTYADDTIVLSSDILA	6	NENYLKTFSDWADKWGISVNAARKGH	25	ESKQSYLVGIL				
Se_p123	GIRYQYNVLPQGWKGSIPAIFQSSMTKILEPFFKQK	4	IYQYMDLLVVGSDLEIG	1	HRTKIEELRQHLLRWGLTTPDKKHQK	0	EPPFLMMAITL				

Figure 5



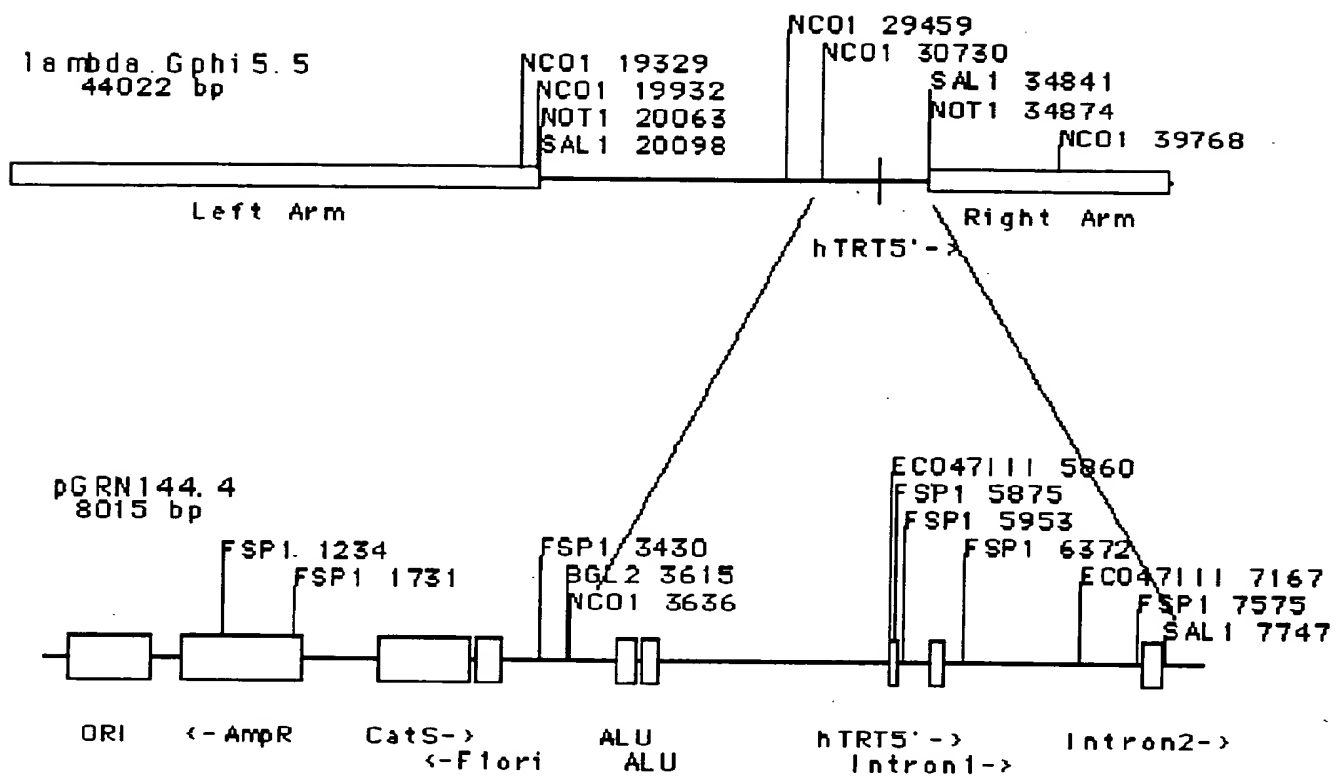
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Figure 6



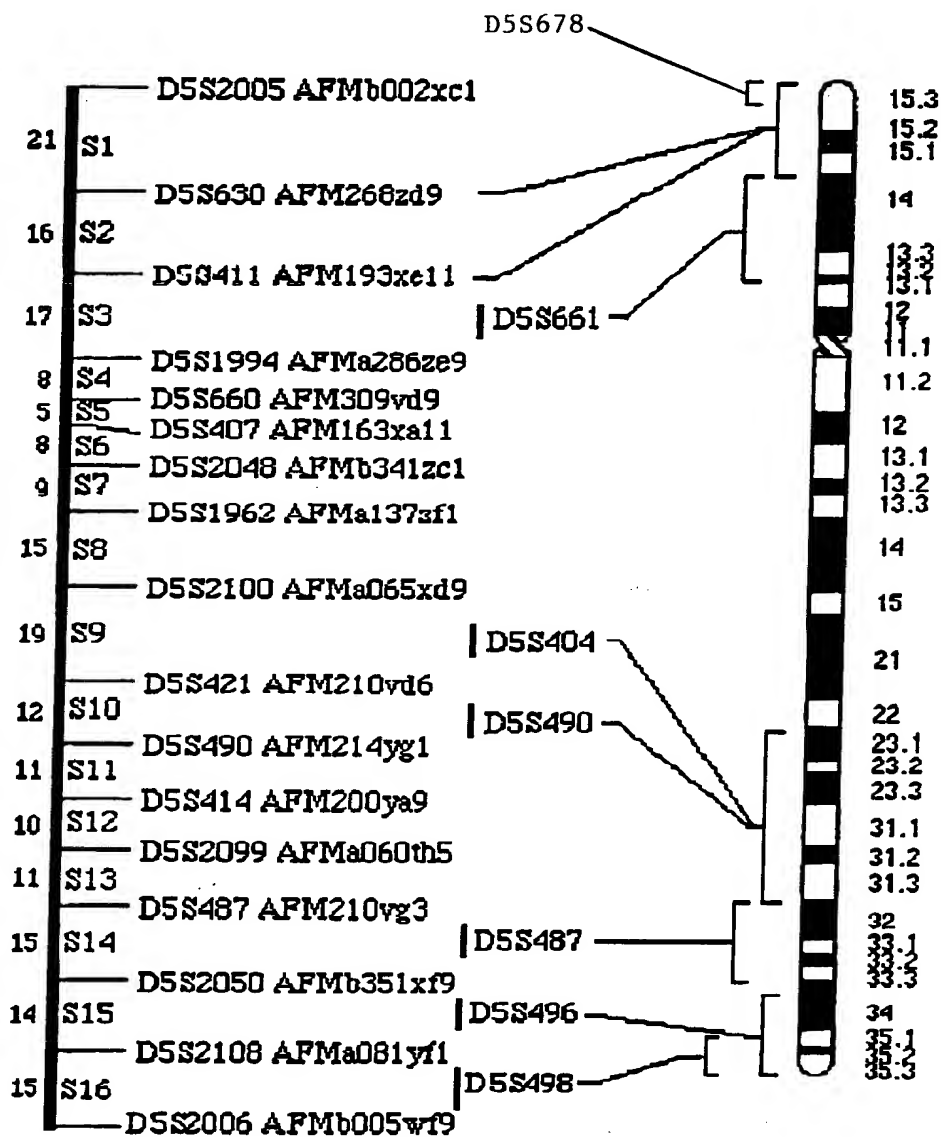
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Figure 7



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Figure 8



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FIGURE 9

Promoter Reporter Construct

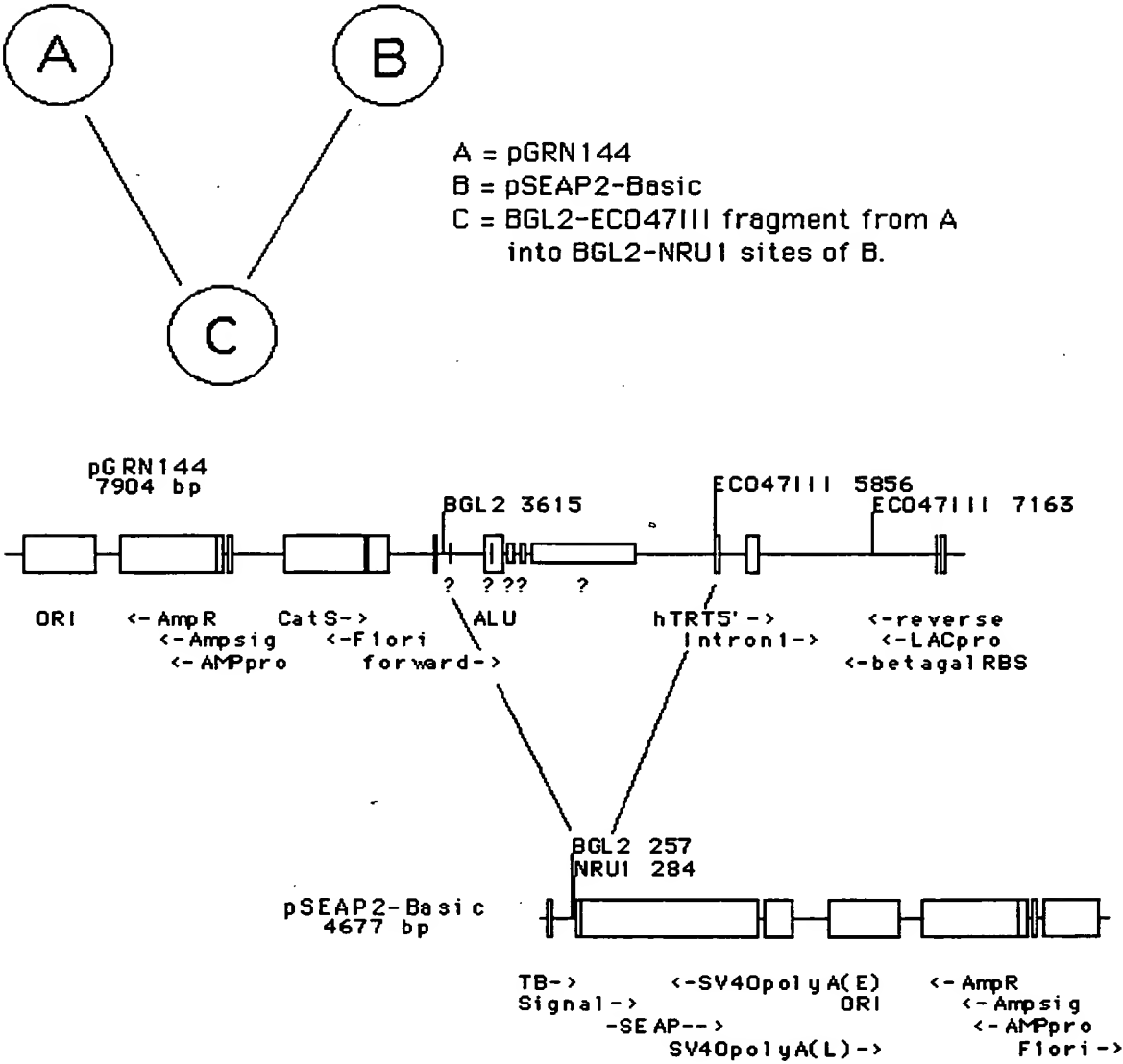
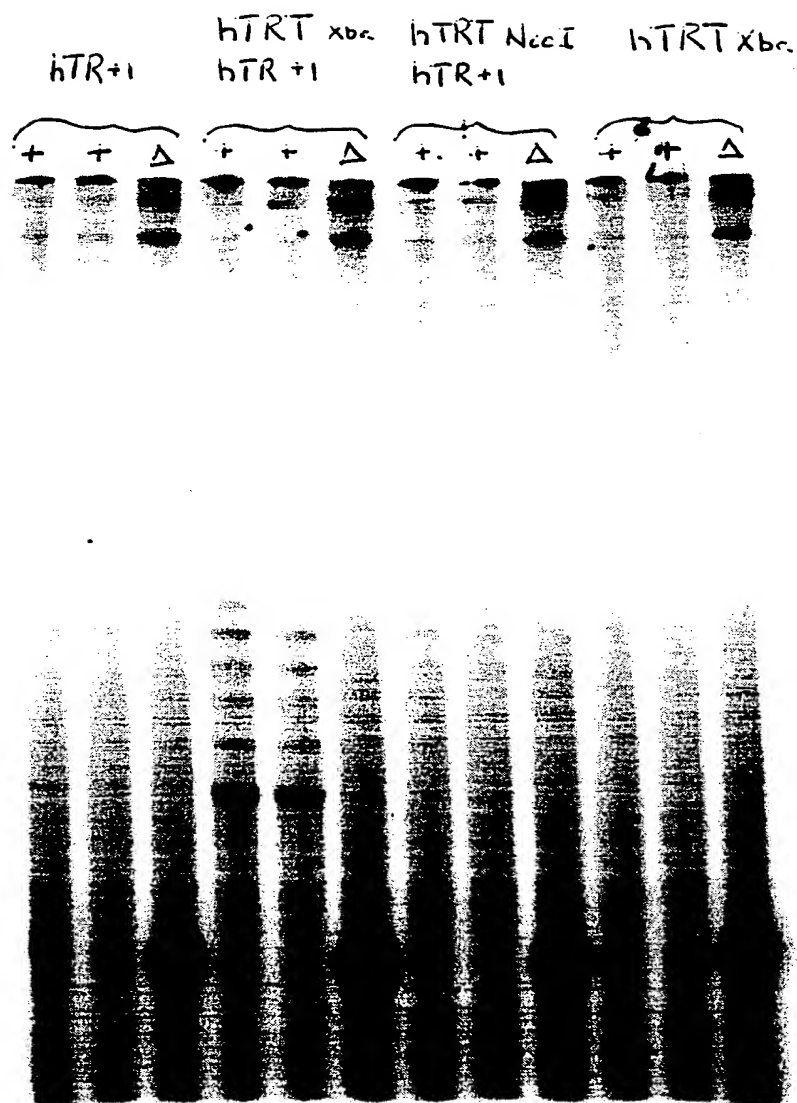
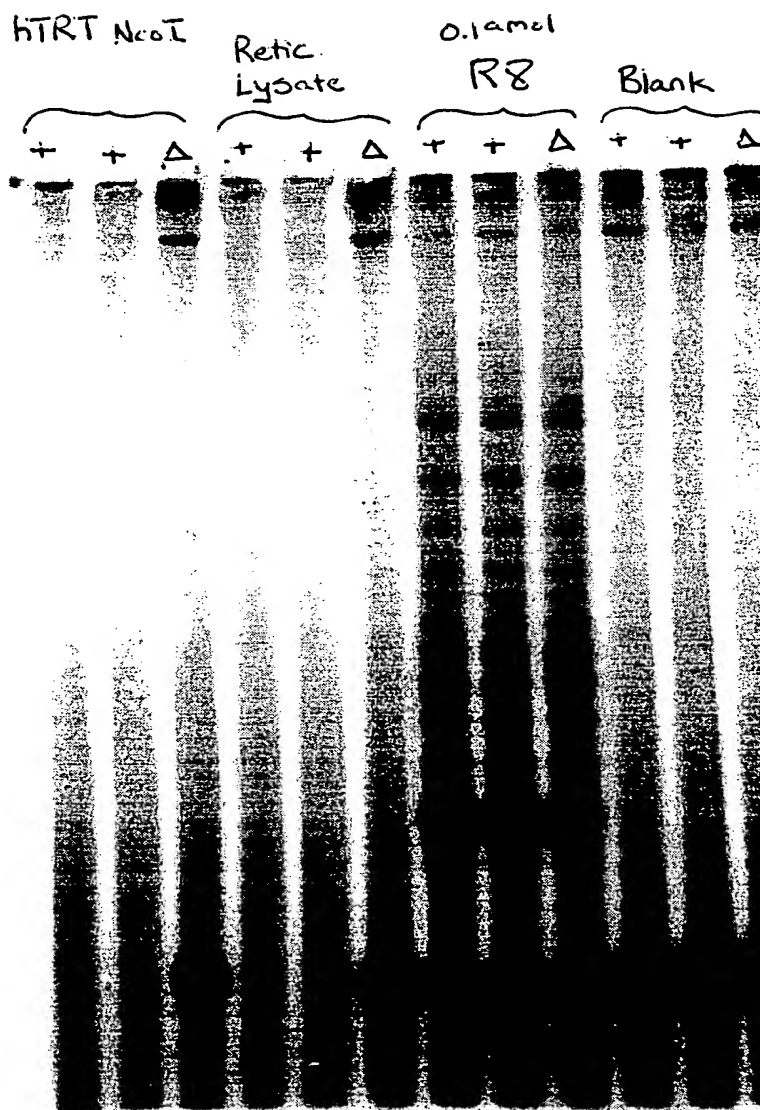


Figure 10  
Page 1



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Figure 10  
Page 2



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FIGURE 11.

Page 1

## Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	WL	
hTRT	FFY TE	E V
spTRT	Y Rk W l I	I
Ea_p123	546 WLMsVYVVELLRsFFYVTETTFQKNRLFFYRKSWSKLQSIGI	13 EAEVR
Sc_Est2	429 WLYNSFIIPILQsFFYITESsDLNRNRTVYFRKDIWKLICRPFI	12 ENNVR
	441 WIFEDLVSLIRCFFYVTEQQKSYSKTYRKNIDVIMKMSI	12 EKEVE
	366 WLFRLIPKIIQTFFYCTEISSTVT.IVYFRHDTWNKLITPFI	9 ENNVC

## Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D cyD i	Y q GipQGs lS l
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGSILSTLLCSLCY	
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPOGSILSSFLCHFYM	
Ea_p123	10 GKLRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSILSSFY	
Sc_Est2	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI	85 YIREDGLFQGSLSAPIVDLVI	
RT con	p hh h K	hR h	h hDh AF h	hPQG pp hh h
			GY	

FIGURE 11  
Page 2

# Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E
TRT con	lllrl DDfL it	g n K	w g s l
hTRT	15 LLLRLVDDFLLVT	15 GVPEYGCVVNLRKTVV	24 WCGLLLDTRTL
spTRT	16 VLLRVVDDFLFIT	15 GFEKHNFSTSLEKTVI	22 FFGFSVNMRSLSL
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGFKFNMKKLQT	28 WIGISIDMKTL
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNAPANRDKILA	25 WKHSSTMNNFH
RT con	h Y DDhhh	Gh h cK h	hLG h
	F		

FIGURE 12

181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  
CCTGGGCCGCGCGAAAGGCGCGGACCACCGGGTCACGGACCACACGCACGGGACCCTGCG

NFkB\_CS1  
GGGRQTYYYQC  
NFkB-MHC-I.2  
TGGGCTTCCCC

241 ACGGCCGCCCCCGCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG  
TGCCGGCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC  
CGACCCCAACTCCCGCCGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB\_CS1  
GGGRQTYYYQC  
NFkB\_CS2  
RGGGRMTYYCC

Topo\_II\_cleavage\_site  
RNYNNCNGYNGKTNINY

\*\*\*\*\*>

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG  
TCCCGCGAAGGGGGCGTCCACAGGACGGAATTCTCGACCACCGGGCTCACGACGTCTCC

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# Figure 13

Page 1

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT  
51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA  
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTAAGTACAGC  
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA  
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT  
251 TTAGAAGATA TTAAAATATT TGCAGCAGACA AATATTGTTG CTACTCCACG  
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAAGTTCTT  
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC  
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA  
501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA  
601 GCGAAGTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG  
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA  
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA  
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT  
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT  
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA  
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG  
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG  
1051 TCCTCTTCCA GAAAATTGGC GGAACGGAA AAAAAAATC GAAAAGTTGA  
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC  
1151 TACACAAGT ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA  
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTT  
1251 AAAAGAAAGT TAAGAAATAT GTGGAAGTAA ACAAGCATGA ACTCATTAC  
1301 AAAAAGTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
1351 GGTGAGACC TCTGCAAGC ATTTTATTA TTTTGATCAC GAAAACATCT  
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG  
1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA  
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT  
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG  
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC GAAGTTATTG  
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC  
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG  
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA  
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAAGTATC  
1951 AACATTCTTA AAAAGTACTA AATTACTTTC TTCAGATTTT TGGATTATGA  
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC  
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT  
2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG  
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA  
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG  
2251 CCAATATAAT TACATTAAGT TTAATGGGAA GTTTTATAAA CAAACAAAAG  
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

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# Figure 13

Page 2

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC  
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACCTCT  
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG  
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

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Figure 14

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD  
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAM  
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH  
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWT FEDLVVS  
451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV  
501 EEWKKS LGFA PGKLR LIPKK TTFRPIMTFN KKI VNSDRKT TKLTNTKLL  
551 NSHLM LKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNVIDSKN  
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ  
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY  
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL  
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTALM PNINLRIEGI LCTLNLMQT KKASMWLKKK LKSFLMNNIT  
901 HYFRKTTTTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID  
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK  
1001 KYTFNRVCM I LKAKEAKLKS DQCQSLIQYD A

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# Figure 15

Page 1

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1 ggtaccgattttacttttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
81 actcaataacaataaccaagtcaaattccaatatgaagggtgttatttagtgatcgataaatatttctattttatcggtcgta 160
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240
241 ggttcgcttacttttaacgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgctcattggatat 320
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcctgcatattc 400
401 ttaacatggagccttacacttttagatgagtcacgtcgcgatgatggagtatttgggtatcatccaacgcttgccctgaaaag 480
481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagttttttgatgcttgcacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctatttctcatgttgtt 640
641 ccaaatatgtatcatctcgtatttaggcttttttccggttttactcctggaatcgtaccttttttactattccccctaata 720
721 ataactctaaattagtttcgcttataattgatagtagtagaaaagatttgggtgattctactcgtgtaattgttattagtttaa 800
801 gatactttgcaaaacatttatttagctatcattatataaaaaaaaaatcctataattataaaatattaatcaatatttgcggtc 880
881 actattttattttaaacgcttatgatcagtaggacactttgcatatatatagtttatgcttaatgggttacttgaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
    1 M  T  E  H  H  T  P  K  S  R  I  L  R  F  L  E  N  Q  Y  V  20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
    21 Y  L  C  T  L  N  D  Y  V  Q  L  V  L  R  G  S  P  A  S  S  40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
    41 Y  S  N  I  C  E  R  L  R  S  D  V  Q  T  S  F  S  I  F  L  60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
    61 H  S  T  V  V  G  F  D  S  K  P  D  E  G  V  Q  F  S  S  P  80

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# Figure 15

Page 2

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgattttttttctattcgggacagctaatatatgggcag 1272  
81 K C S Q S E 86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332  
87 L I A N V V K Q M F D E S F E R R R N L 106

1333 CTG ATG AAA GGG TTT TCC ATG gtaagggtatttctaattgtgaaatattttacctgcaattactgttttcaaagaga 1405  
107 L M K G F S M 113

1406 ttgtattttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469  
114 N H E D F R A M H V N G V Q N 128

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529  
129 D L V S T F P N Y L I S I L E S K N W Q 148

1530 CTT TTG TTA GAA AT gtaaataaccgggttaagatgttgcgacattttgaacaagactgacaagtatag T ATC GGC 1601  
149 L L L E I I G 155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661  
156 S D A M H Y L L S K G S I F E A L P N D 175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721  
176 N Y L Q I S G I P L F K N N V F E E T V 195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781  
196 S K K R K R T I E T S I T Q N K S A R K 215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841  
216 E V S W N S I S I S R F S I F Y R S S Y 235

1842 AAG AAG TTT AAG CAA G gtaactaataactgtttatcccttcataactaatttttag AT CTA TAT TTT AAC  
1907

236 K K F K Q D L Y F N 245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967  
246 L H S I C D R N T V H M W L Q W I F P R 265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027  
266 Q F G L I N A F Q V K Q L H K V I P L V 285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087  
286 S Q S T V V P K R L L K V Y P L I E Q T 305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147  
306 A K R L H R I S L S K V Y N H Y C P Y I 325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207  
326 D T H D D E K I L S Y S L K P N Q V F A 345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267  
346 F L R S I L V R V F P K L I W G N Q R I 365

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336  
366 F E I I L K D L E T 375

# Figure 15

Page 3

2337	TTC	TTG	AAA	TTA	TCG	AGA	TAC	GAG	TCT	TTT	AGT	TTA	CAT	TAT	TTA	ATG	AGT	AAC	ATA	AAG	2396																
376	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	N	I	K	395																
2397	gtaatatgccaaatttttttaccattaattaacaatcag																			ATT	TCA	GAA	ATT	GAA	TGG	CTA	GTC	CTT	GGA	2465							
396																				I	S	E	I	E	W	L	V	L	G	405							
2466	AAA	AGG	TCA	AAT	GCG	AAA	ATG	TGC	TTA	AGT	GAT	TTT	GAG	AAA	CGC	AAG	CAA	ATA	TTT	GCG	2525																
406	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	Q	I	F	A	425																
2526	GAA	TTC	ATC	TAC	TGG	CTA	TAC	AAT	TCG	TTT	ATA	ATA	CCT	ATT	TTA	CAA	TCT	TTT	TTT	TAT	2585																
426	E	F	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	445																
2586	ATC	ACT	GAA	TCA	AGT	GAT	TTA	CGA	AAT	CGA	ACT	GTT	TAT	TTT	AGA	AAA	GAT	ATT	TGG	AAA	2645																
446	I	T	E	S	S	D	L	R	N	R	T	V	Y	F	R	K	D	I	W	K	465																
2646	CTC	TTG	TGC	CGA	CCC	TTT	ATT	ACA	TCA	ATG	AAA	ATG	GAA	GCG	TTT	GAA	AAA	ATA	AAC	GAG	2705																
466	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	485																
2706	gtattttaaaagtatttttttgcataaagctaataattttcag																			AAC	AAT	GTT	AGG	ATG	GAT	ACT	CAG	AAA	ACT	2775							
486																				N	N	V	R	M	D	T	Q	K	T	495							
2776	ACT	TTG	CCT	CCA	GCA	GTT	ATT	CGT	CTA	TTA	CCT	AAG	AAG	AAT	ACC	TTT	CGT	CTC	ATT	ACG	2835																
496	T	L	P	P	A	V	I	R	L	L	P	K	K	N	T	F	R	L	I	T	515																
2836	AAT	TTA	AGA	AAA	AGA	TTT	TTA	ATA	AAG	gtattaattttttggatcatcaatgtactttactttctaattctatta											2906																
516	N	L	R	K	R	F	L	I	K												524																
2907	ctagcag		ATG	GGT	TCA	AAC	AAA	AAA	ATG	TTA	GTC	AGT	ACG	AAC	CAA	ACT	TTA	CGA	CCT	GTG	2967																
525			M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	542																
2968	GCA	TCG	ATA	CTG	AAA	CAT	TTA	ATC	AAT	GAA	GAA	AGT	AGT	GGT	ATT	CCA	TTT	AAC	TTG	GAG	3027																
543	A	S	I	L	K	H	L	I	N	E	E	S	S	G	I	P	F	N	L	E	562																
3028	GTT	TAC	ATG	AAG	CTT	CTT	ACT	TTT	AAG	AAG	GAT	CTT	CTT	AAG	CAC	CGA	ATG	TTT	GG	gtaat	3088																
563	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G		581																
3089	tatataatgcgcgattccctcattattaatttttgcag																			G	CGT	AAG	AAG	TAT	TTT	GTA	CGG	ATA	GAT	ATA	3155						
582																				R	K	K	Y	F	V	R	I	D	I	591							
3156	AAA	TCC	TGT	TAT	GAT	CGA	ATA	AAG	CAA	GAT	TTG	ATG	TTT	CGG	ATT	GTT	AAA	AAG	AAA	CTC	3215																
592	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	611																
3216	AAG	GAT	CCC	GAA	TTT	GTA	ATT	CGA	AAG	TAT	GCA	ACC	ATA	CAT	GCA	ACA	AGT	GAC	CGA	GCT	3275																
612	K	D	P	E	F	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	631																
3276	ACA	AAA	AAC	TTT	GTT	AGT	GAG	GCG	TTT	TCC	TAT	T	gtaagtttttttttttttcattggaatttttttaacaa								3343																
632	T	K	N	F	V	S	E	A	F	S	Y	F									643																
3344	atttttttttttag																			TT	GAT	ATG	GTG	CCT	TTT	GAA	AAA	GTC	GTG	CAG	TTA	CTT	TCT	ATG	AAA	ACA	3405
644																					D	M	V	P	F	E	K	V	V	Q	L	L	S	M	K	T	659
3406	TCA	GAT	ACT	TTG	TTT	GTT	GAT	TTT	GTG	GAT	TAT	TGG	ACC	AAA	AGT	TCT	TCT	GAA	ATT	TTT	3465																
560	S	D	T	L	F	V	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	679																
3466	AAA	ATG	CTC	AAG	GAA	CAT	CTC	TCT	GGA	CAC	ATT	GTT	AAG	gtataccaattgttgaattgtaataaca							3532																
680	K	M	L	K	E	H	L	S	G	H	I	V	K								692																

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# Figure 15

Page 4

3533	ctaataaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	3593
693		I G N S Q Y L Q K V G I P Q G S	708
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtagattgctgctcattcc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840	
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG	4089	
839	K S F F Y K I L R	848	
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtagtacttattttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagtcattaattaaccccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC	4339	
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgct	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	ggctctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA	4468	
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q S L T	966	
4529	GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA tctcattttcaatttattatatacatcctttattactggtgctcttaacaatattattactaagtata	4665	
987	A D	989	

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Figure 15  
Page 5

4666 gctgacccccaaagcaagcatactataggatttcttagtaaagtaaaattaatctcgttattagcttttgattgacttgtct 4745  
4746 ttatcctttatactttttaagaaagattgacagtgggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825  
4826 ttaaaagtaatacatgaggctaactctcctttcatttagaataaggaaagtgggttttctataatgaataatgcccgcacta 4905  
4906 atgcaaaaagacgaagattatcttctaaacaaggggggattaagcatatccgaaggaaaagagagtaacatacccagtgtt 4985  
4986 gctgaagaaagcaaggataaatttggaacaagcttctgcagatgacaggctaataatttggtgaccgaattttggtaaaagc 5065  
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145  
5146 atgtcttatataagggttttggttttttcttgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225  
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305  
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385  
5386 aaaaaagaaaatattcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465  
5466 acctctatttctgaaatgtatggtcctactgtcgccttcgacttctcgtagctctacgcagcttaagtgaccaaagggtacc 5544

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FIGURE 16  
page 1  
(Seq. ID. No. 1)

1 gcagcgctgc gtccctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc  
61 gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct  
121 gccgctggcc acgttcgtgc ggcgccctggg gcccagggc tggcggttg tgacgcgcg  
181 ggaccgcggc gctttccgcg cgctggtggc ccagtgcctg gtgtgcgtgc cctgggacgc  
241 acggccgccc cccgcccggc cctccttcgg ccaggtgtcc tgccgaagg agctgggtggc  
301 ccgagtgtcg cagaggctgt gcgagcgcg cgcaagaac gtgctggcct tcggcttcgc  
361 gctgctggac gggggccgcg gggggccccc cgaggccttc accaccagcg tgcgcagcta  
421 cctgcccac acggtgaccg acgactgcg ggggagcggg gcgtgggggc tgctgctgcg  
481 ccgctggggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt  
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcccgtg taccagctcg gcgctgccac  
601 tcaggcccgg ccccccggcc acgctagtgg accccgaagg cgtctgggat gcgaacgggc  
661 ctggaacat agcgtcaggg aggcgggggt cccctggggc ctgccagccc cgggtgcgag  
721 gaggcgcggg ggcagtgcca gccgaagtct gccgttgccc aagaggccca ggcgtggcgc  
781 tgcccctgag ccggagcgga cgcccgttg gccaggggtcc tggggccacc cgggcaggac  
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccgg ccgaagaagc  
901 cacctctttg gaggggtgcg tctctggcac gcgccactcc caccatccg tgggcccga  
961 gcaccacgcg gggcccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc  
1021 cccggtgtac gccgagacca agcacttctc ctactcctca ggcgacaagg agcagctgcg  
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggctcgtgga  
1141 gaccatcttt ctgggttcca ggccctggat gccagggact cccgcaggt tgccccgct  
1201 gccccagcgc tactggcaaa tgcggccctt gtttctggag ctgcttggga accacgcgca  
1261 gtgcccctac ggggtgctcc tcaagacgca ctgcccgtg cgagctgcgg tcaccccagc  
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg aggaggagga  
1381 cacagacccc cgctgcctgg tgcagctgct ccgccagcac agcagccctt ggcaggtgta  
1441 cggtctcgtg cgggcctgcc tgcgcccgtt ggtgccccca ggctctggg gctccaggca  
1501 caacgaacgc cgcttctca ggaacaccaa gaagttcatc tcctgggga agcatgccaa  
1561 gctctcgtcg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgcag  
1621 gagcccaggg gttggctgtg ttccggccgc agagcacctg ctgctgagg agatcctggc  
1681 caagttcctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta  
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag  
1801 caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc  
1861 ggaagcagag gtcaggcagc atcgggaagc caggcccggc ctgctgacgt ccagactccg  
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc  
1981 cagaacgttc cgagagaaa agagggccga gcgtctcacc tcgagggtga aggcactgtt  
2041 cagcgtgctc aactacgagc gggcgcgcg ccccggcctc ctgggcgcct ctgtgctggg  
2101 cctggacgat atccacagg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc  
2161 gccgctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccca  
2221 ggacaggctc acggaggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg  
2281 tcggtatgcc gtggtccaga aggcggccca tgggcacgtc cgcaaggcct tcaagagcca  
2341 cgtctctacc ttgacagacc tccagccgta catgacagag ttcgtggctc acctgcagga  
2401 gaccagcccg ctgagggatg ccgtcgtcat cgagcagagc tcctccctga atgaggccag  
2461 cagtggcctc ttgcagctct tctacgctt catgtgccac cacgcccgtg gcacagggg  
2521 caagtcctac gtccagtgc aggggacccc gagggtctc atcctctcca cgtgctctg  
2581 cagcctgtgc taggctgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct  
2641 gctcctgcgt ttggtggatg atttcttggt ggtgacacct cacctaccc acgcgaaac  
2701 cttcctcagg accctggctc gaggtgtccc tgagtatggc tgcgtgggtg acctgaggaa  
2761 gacagtgggt aacttccttg tagaagacga ggccctgggt ggcacggctt ttgttcagat  
2821 gccggcccac ggccatttcc cctggtgcgg cctgctgctg gatacccga ccctggaggt  
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca cttcaaccg

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FIGURE 16  
page 2  
(Seq. ID. No. 1)

2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg  
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta  
3061 caagatcctc ctgctgcagg cgtacagggt tcacgcatgt gtgctgcagc tcccatttca  
3121 tcagcaagtt tggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct  
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctggggggcca agggcgccgc  
3241 cggccctctg ccctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct  
3301 gactcgacac cgtgtcacct acgtgccact cctgggggtca ctcaggacag cccagacgca  
3361 gctgagtcgg aagctcccgg ggacgacgct gactgccctg gaggccgcag ccaaccgggc  
3421 actgccctca gacttcaaga ccatcctgga ctgatggcca cccgcccaca gccaggccga  
3481 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg agggcgggcc  
3541 cacaccagg cccgcaccgc tgggagtctg aggcctgagt gagtgtttgg ccgaggcctg  
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaaaggct  
3661 gagtgtccag cacacctgcc gtcttcaact cccacaggc tggcgctcgg ctccacccca  
3721 gggccagctt ttctcacca ggagcccggc ttccactccc cacataggaa tagtccatcc  
3781 ccagattcgc cattgttcac ccctgcacct gccctccttt gccttccacc cccaccatcc  
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgtg caaagggtgtg  
3901 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg  
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

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FIGURE 17  
HUMAN TRT PROTEIN SEQUENCE  
(SEQ. NO. 2)

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP  
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFA  
LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV  
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA  
PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPA  
RPAAEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS  
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPL  
FLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQ  
LLRQHSSPWQVYGFVRACLRLRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQEL  
TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET  
TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFI  
PKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLG  
LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC  
VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL  
NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGD MENKLFAG  
IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFVVEDEAL  
GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRR  
KLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPT  
FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLCLKLTRHRT  
YVPLLGSLRTAQTQLSRKLP GTTTLTALEAAANPALPSDFKTILD

464130" T562T680

**FIGURE 18**  
Clone 712562  
(SEQ ID NO. 3 )

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT  
TTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTG  
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACAGCTGCGGGAGCT  
GTCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT  
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGG  
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT  
GTTGAGCGTGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT  
GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGA  
CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC  
CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT  
GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAG  
CCACGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT  
GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTTCGGCGGGACGGGC  
TGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA  
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGA  
AGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTTCA  
TGCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGG  
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC  
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTTGGGGTCTTGCGGCTGAAGT  
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT  
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTT  
ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC  
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG  
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC  
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC  
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCAACCCGG  
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG  
AGAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCAGGGAGGGAGGGCGGC  
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCT  
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC  
TGAGTGTCCAGCACACCTGCCGTCTTCACTCCCCACAGGCTGGCGCTCGGCTCCACCCC  
AGGGCCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATC  
CCCAGATTCGCCATTGTTTCAACCCCTCGCCCTGCCCTCCTTTGCCCTTCCACCCCCACCATC  
CAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT  
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGG  
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTG0AAAAAAAAAA  
AAAAAAAAAAAAAAAAAA

00012562.03149

FIGURE 19

SEQ ID NO. 10

MetSerValTyrValValGluLeuLeuArgSerPhePhe  
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrp  
SerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeu  
SerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeu  
ArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGly  
AlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeu  
PheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeu  
GlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAsp  
ProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIlePro  
GlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysVal  
ArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSer  
HisValLeuArgProValProGlyAspProAlaGlyLeuHisProLeuHisAlaAlaLeu  
GlnProValLeuArgArgHisGlyGluGlnAlaValCysGlyAspSerAlaGlyArgAla  
AlaProAlaPheGlyGly

464T30" T562T630

Page 1

SEQUENCE NO. 4 (DNA) AND SEQUENCE NO. 5 (PROTEIN)  
(TRANSLATION OF A  $\Delta 182$  hTRT VARIANT)

1

met

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

30

his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50

60

phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80

90

leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110

120

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

# FIGURE 20

Page 2

130

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140

trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

150

160

leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

180

190

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200

leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

210

220

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

240

250

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

270

00552T580

## Page 3

290 300

gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330

trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390

arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400

leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

			410										420		
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro	
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA	

430

# FIGURE 20

Page 4

ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440

450

ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460

leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CCG

470

480

ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490

his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500

510

leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520

met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530

540

gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550

ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560

570

leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580

arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

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# FIGURE 20

Page 5

590 600  
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610  
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
 pro ile val asn met asp tyr val val gly ala arg thr phe arg  
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

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# FIGURE 20

Page 6

740

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750

760

his gly his val arg lys ala phe lys ser his val leu arg pro  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770

val pro gly asp pro ala gly leu his pro leu his ala ala leu  
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

780

790

gln pro val leu arg arg his gly glu gln ala val cys gly asp  
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800

807

ser ala gly arg ala ala pro ala phe gly gly OP  
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA  
GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGC  
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT  
GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC  
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA  
ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAG  
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA  
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCT  
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG  
GATGTCGCTGGGGGCCAAGGGCGCCGCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT  
GTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT

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# FIGURE 20

Page 7

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC  
TGCCCTGGAGGCCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG  
ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGGCT  
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG  
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGCTGAG  
GCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCAGCACACCTGCCGTCTTCACTTCCC  
CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC  
CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTTACCCCTCGCCCTGCC  
CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC  
TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT  
GGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG  
AGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0891251.031497  
464TBD 1562T680

## page 1

3601 ATCGATTGGGCCCCGAGATCTCGCGCGCGAGGCCTGCCATGGGACCCACTGTCAGGGGCAGC  
TAGCTAACCCGGGCTCTAGAGCGCGCGCTCCGGACGGTACCCTGGGTGACGTCCTCCCGTCG

3636  
NCO1

3841 CCCCCAGGGGCAGAGGAGTTCCTCTCACTCCTGTGGAGGAAGGAATGATACTTTGTATT  
GGGGGTCCCGTCTCCTCAAGGAGAGTGAGGACACCTCCTTCCTTACTATGAAACAATAA

\*\*\*\*\*

3901 TTTCAGTCTGGTACTGAATCCACTGTTTCATTTGTTGGTTTGTGTTGTTTGTGTTTGTGAGAA  
AAAGTGACGACCATGACTTAGGTGACAAAGTAAACAACCAAACAAACAAAACAAAACCTCT

\*\*\*\*\*

3961 AGCGGTTTCACTCTTGTTGCTCAGGCTGGANGGAGTGCAATGGCGCGATCTTGGCTTACT  
TCGCCAAAGTGAGAAACAAGAGTCCGACCTNCCTCACGTTACCGCGCTAGAACCGAATGA

ALU

\*\*\*\*\*

4021 GCAGCCTCTGCCTCCCAGGTTCAAGTGATTCTCCTGCTTCCGCCTCCCATTTGGCTGGGA  
CGTCGGAGACGGAGGGTCCAAGTTCACTAAGAGGACGAAGGCGGAGGGGTAAACCGACCCCT

\*\*\*\*\*

\*\*\*\*\*

4081 TTACAGGCACCCGCCACCATGCCCAGCTAATTTTTTGTATTTT TAGTANANACNGGGGTG  
AATGTCCGTGGGCGGTGGTACGGGTCGATTAAAAAACATAAAAATCATNTNTGNCCCCAC

A

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4141 GGGGTGGGGTTCACATGTTGGCCAAGCTGGTCTCGAACTTCTGAACTCAGATGATCCANC  
CCCCACCCCAAGTGTAACAACCGGTTGACCAGAGCTTGAAGACTTGAGTCTACTAGGTNG

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4201 TGCCTCTGCCTCCTAAATTGCTGGGATTACAGGTGTNANCCACCATGCCCAACTCAAAA

# FIGURE 21

page 2

ACGGAGACGGAGGATTTTAACGACCCTAATGTCCACANTNGGTGGTACGGGTTGAGTTTT

4261 TTTACTCTGTTTANAAACATCTGGGTCTAAGGTAGGAANCTCACCCCACTCAATTTTTGT  
AAATGAGACAAATNTTTGTAGACCCAGATTCCATCCTTNGAGTGGGGTGAGTTAAAAACA

4321 GGTGTTTTTAAGCCAATNANAAAATTTTTTNATGTTGTTTNNNNNNNNNNNNNNNNNNNN  
CCACAAAATTCGGTTANTNTTTTAAAAAANTACAACAAANNNNNNNNNNNNNNNNNNNNNN

4381 NNN  
NN

4441 NNN  
NN

4501 NNN  
NN

4561 NNN  
NN

4621 NNN  
NN

4681 NNN  
NN

4741 NNN  
NN

4801 NNN  
NN

4861 NNN  
NN

4921 NNN  
NN

4981 NNN  
NN

5041 NGCCANGRAGGGGGCCAGGTTCCAANTTCCCAACCKTTTTWGGARGGACNGCCCCCAGGG  
NCGGTNCYTCCCCCGGTCCAAGGTTNAAGGGTTGGMAAAWCCCTYCCTGNCGGGGGTCCC

5101 GGGGATRAACAGANTNGGGGGKGGTWGGGTTNAKGGTGGGAACNCCTTNGCGCCTGGAG  
CCCCTAYTTGTCTNANCCCCMCCAWCCCAANTMCCACCCTTGNGGAANCGSCGGACCTC

5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGGCGGGGRAGTTTG  
TTGCACGTTTCTCCTTTACTTCCCGGACMCAGTTCCTCGGGTTCANCCGCCCCYTCAAAC

08912951.081497

# FIGURE 21

page 3

5221 CAGGGAGGCACTCCGGGGAGGTCCSGCGTGCCCGTCCAAGGGAGCAATGCGTCCTTCGGG  
GTCCCTCCGTGAGGCCCTCCAGGSCGCACGGGCAGGTTCCCTCGTTACGCAGGAAGCCC

5281 TTCGTCCCCAWGCCGCGTCTACGCGCTYCCGTCTCCCTTCACGTTCCGGCATTTCGTG  
AAGCAGGGGTWCGGCGCAGATGCGCGGARGGCAGGAGGGGAAGTGCAAGGCCGTAAGCAC

5341 GTGCCCCGAGCCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG  
CACGGGCCTCGGGCTGCGGGGCGCAGGCCCTGGACCTCCGTGCGGGACCCAGAGGCCTAGTC

5401 GCCAGCGGCCAAAGGGTCGCGGCACGCACCTGTTCCAGGGCCTCCACATCATGGCCCCCT  
CGGTGCGCGGTTTCCAGCGGCGTTCGTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

5461 CCCTCGGGTTACCCACAGCCTAGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCGCCT  
GGGAGCCCAATGGGGTGTTCGATCCGGCCTAAGCTGGAGAGAGGCGACCCGGGAGCGGA

Sp1

\*\*\*\*\*

5521 GCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCCATACCC  
CCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCGCCCTTCGCGCCGGGTATGGG

5581 CCGGGTCCGCCCCGAAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTGGATTTCG  
GGCCAGGCGGGCCTTCGTGACGCGACAGCCCCGGTCCGGCCCGAGGGTCACCTAAGCG

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5641 GGGCACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAAGGACTGGGGACCCGGGCACC  
CCCGTGTCTGCGGGTCTGGCGCGAAGGGTGACCGCCTTCCTGACCCCTGGGCCCCGTGG

E2F

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5701 CGTCCTGCCCCCTTACCTTCCAGCTCCGCTTCTTCCGCGCGGACCCGGCCCCGTCCCGAA  
GCAGGACGGGGAAGTGGAAGGTCGAGGCGAAGAAGGCGCGCTGGGCCGGGGCAGGGCTT

E

\*\*\*\*

5761 CCCTTCCAGGTCCCGGCCAGCCCCCTTCGGGGCCCTCCAGCCCCCTCCCTTCTTTT  
GGGAAGGGTCCAGGGCCGGGTGCGGGAAGGCCGGGAGGGTCGGGGAGGGGAAGGAAAAG

0847168157

# FIGURE 21

page 4

Sp1

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2F

NFkB

h

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5821 CGCGGCCCCGCCCTCTCCTTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCA  
GCGCCGGGGCGGGAGAGGAAGCGCCGCGCTCAAAGTCCGTCGCGACGCAGGACGACGCGT

5860

ECO47III

5875

FSP1

TRT5'

\*\*\*\*\*>

5881 CGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCG  
GCACCCTTCGGGACCGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTCGGC

5941 TGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGCGGC  
ACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACGCCG

5953

FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGC  
CGGACCCCGGGTCCCAGCCGCCGACACGTCGCGCCCCCTGGGCCCGCGAAAGGCGCGC

6061 TGGTGGCCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCCGCCCCCT  
ACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGCGGCGGGGGA

NFkB

=====

\*\*\*\*\*

6121 CCTTCCGCCAGGTGGGCCTCCCCGGGGTCCGGCTCCGGCTGGGGTTGAGGGCGGCCGGGG  
GGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGAGGCCGACCCAACTCCCGCCGGCCCC

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::::::::::::::::::

NFkB

=====

Intron1

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6181 GGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTC  
CCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCACAG

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# FIGURE 21

page 5

6241 CTGCCTGAAGGAGCTGGTGGCCCGAGTGTCTGCAGAGGCTGTGCGAGCGCGGCGGAAGAA  
GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTT  
GCACGACCGBAAGCCGAAGCGCGACGACCTGCCCCGGGCGCCCCGGGGGGGCTCCGGAA

6361 CACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGG  
GTGGTGGTTCGACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTCGCC

6372

FSP1

6421 GCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACG  
CCGCACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGC

6481 CTGCGCGCTCTTTGTGCTGGTGGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCT  
GACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCCGGCGGCGA

6541 GTACCAGCTCGGCGCTGCCACTCAGGCCCGGGCCCCGCCACACGCTAGTGGACCCCCGAAG  
CATGGTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGCTTC

6601 GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGG  
CGCAGACCTTACGCTTGCCCCGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCC  
GGACGGTCGGGGGCCACGCTCCTCCGCGCCCCCGTACGGTTCGGCTTCAGACGGCAACGG

6721 CAAGAGGCCCCAGGCGTGGCGCTGCCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGGGTC  
GTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAG

6781 CTGGGCCCCACCGGGCAGGACGCGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTACC  
GACCCGGGTGGGCCCCGTCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAGTGG

6841 TGCCAGACCCGCCGAAGAAGCCACCTCTTTGAGGGTGCGCTCTCTGGCACGCGCCACTC  
ACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGTGAG

6901 CCACCCATCCGTGGGCGGCCAGCACGCGGGCCCCCATCCACATCGCGGCCACCACG  
GGTGGGTAGGCACCCGGCGGTTCGTGGTGCGCCCGGGGGTAGGTGTAGCGCCGGTGGTGC

6961 TCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCCTC  
AGGGACCCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTTCGTGAAGGAGATGAGGAG

7021 AGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGAC  
TCCGCTGTTCTCTGTCGACCGCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTTCGGACTG

7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGAC  
ACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCCCTG

6521-6540

# FIGURE 21

page 6

7141 TCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGGCCCCTGTTTCTGGA  
AGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGACCT

7167

ECO47III

7201 GCTGCTTGGGAACACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGCT  
CGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGGCGA

7261 GCGAGCTGCGGTACCCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGT  
CGCTCGACGCCAGTGGGGTCGTGCGCCACAGACACGGGCCCTCTTCGGGGTCCCAGACA

7321 GGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCA  
CCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCAGCGACCACGTCGACGAGGCGGTCTGT

7381 CAGCAGCCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCC  
GTCGTGCGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGGGGG

7441 AGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCAT  
TCCGGAGACCCCCAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTA

7501 CTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG  
GAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCGACTGCACCTTCTACTCGCACGC

\*\*\*\*\*

7561 GGA CTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCCAGG  
CCTGACGCGAACCAGCGCTCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGGTCC

7575

FSP1

Intron2

\*\*\*\*\*

7621 CCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCTCCT  
GGGGTCTCGACTTACGTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGAGGA

\*\*\*\*\*

7681 GTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTGAGTGGACACGGTG  
CAGAGGTAGCAGTGACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGCCAC

\*\*>

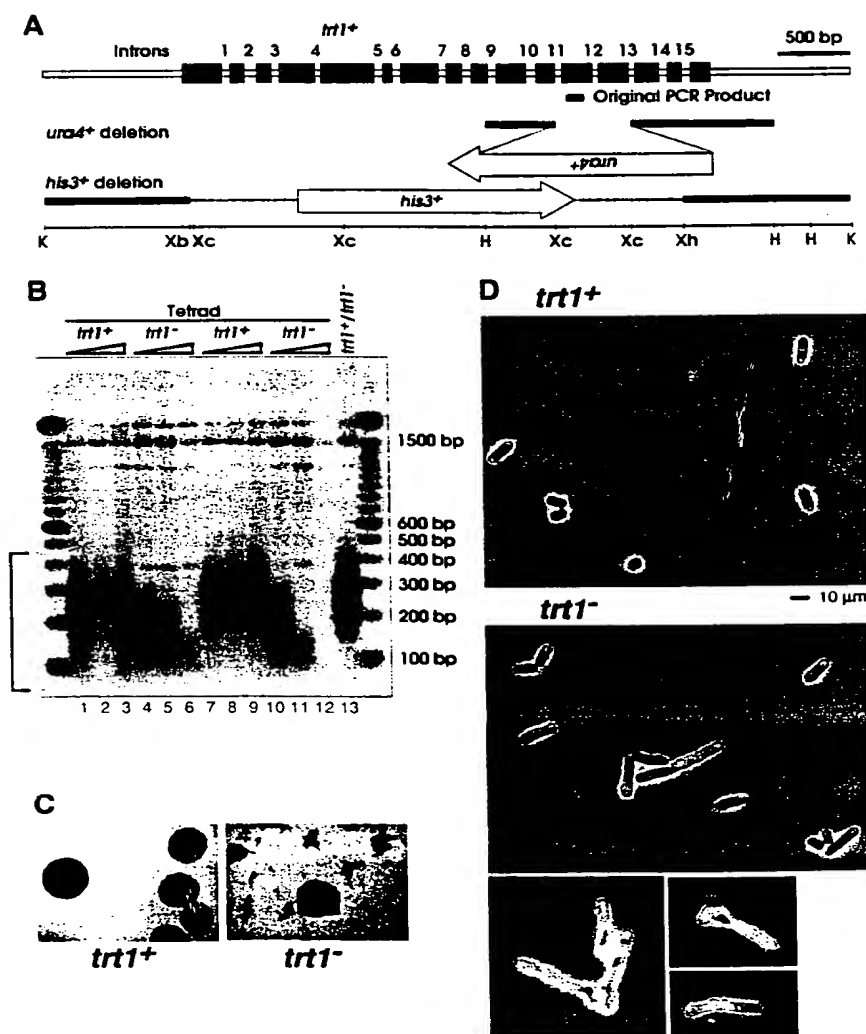
7741 ATCGAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTTCGTAATCATGGTCATA  
TAGCTCCAGCTGAGATCTCCTAGGGGCCCATGGCTCGAGCTTAAGCATTAGTACCAGTAT

7747

SAL1

64T30" T55T60



[illegible]

**FIGURE 23**  
EST AA281296  
(Seq. ID. No. 8)

gc  
caagttcctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta  
tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag  
caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggacgtgtc  
ggaagcagag gtcaggcagc atcggaagc caggcccgcc ctgctgacgt ccagactccg  
cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc  
cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactgtt  
cagcgtgctc aactacgagc gggcgcg

08912961.031497

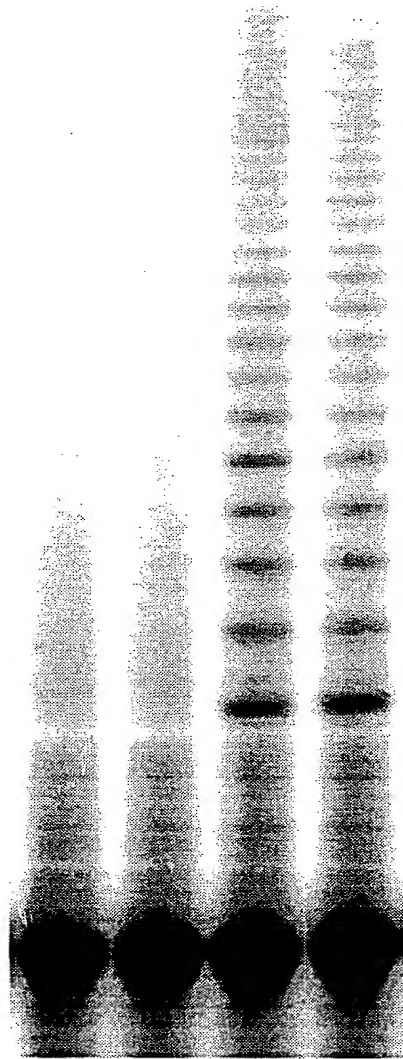
FIGURE 24  
(Seq. ID. No. 9)

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG  
ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGC  
CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCAT  
CAGGGGCAAGTC

00912951-081497

Figure 25

pBBS212 pGRN133



← INTERNAL CONTROL

approximate cell # 5,000 5,000 5,000 5,000

08912951 081497